

Conor R. Walker

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Education

University of Cambridge, UK

2017-Present

PhD in Computational Biology · expected Q4 2021

- Thesis (submitted): Statistical analysis of short template switch mutations in human genomes
- Advisers: Nick Goldman, Aylwyn Scally
- Committee: Zamin Iqbal, Jan Korbel

Newcastle University, UK

2016-2017

MSc Bioinformatics · first-class honours (83%)

- Thesis: Optimising nucleic acid sequences for DNA strand displacement systems
- Adviser: Harold Fellermann

Liverpool John Moores University, UK

2013-2016

BSc (Hons) Zoology · first-class honours (80%)

- Thesis: The genetics of insecticide resistance in the blackfly *Simulium vittatum*
- Advisers: Craig Wilding, Will Swaney

Research experience

EMBL - European Bioinformatics Institute, UK

2017-Present

Predocutorial Researcher · Adviser: Nick Goldman

- I have developed statistical methods to identify template switch variants in DNA sequences
- I have characterised the human evolutionary, population, and cancer landscape of template switch mutagenesis
- I have designed convolutional neural networks for accurately detecting between-species positive selection, validated through large-scale simulation of training and testing data
- I processed large collections of SARS-CoV-2 sequencing data, from which our group has produced a community resource that is used in ongoing global pandemic phylogenetic analyses

This work was funded by both EMBL and NIHR BRC.

Newcastle University, UK

2016-2017

Postgraduate Student Research

- I implemented multi-objective genetic algorithms for designing and optimising DNA sequences for use in DNA computing systems

Liverpool John Moores University, UK

2016

Undergraduate Student Research

- I identified enzyme families and point mutations associated with insecticide resistance in a medically-important blackfly genome using phylogenetic methods

Research Assistant

2014-2016

- I processed nematode samples from across the UK for sequencing using various molecular biology protocols in a wet lab environment

Publications

Peer-reviewed

Mutation rates and selection on synonymous mutations in SARS-CoV-2.

De Maio N., Walker C. R., Turakhia Y., Lanfear R., Corbett-Detig R., Goldman N.

[Genome Biology and Evolution](#) 13, evab087 (2021).

Short-range template switching in great ape genomes explored using pair hidden Markov models.

Walker C. R., Scally A., De Maio N., Goldman N.

[PLOS Genetics 17, e1009221](#) (2021).

Stability of SARS-CoV-2 phylogenies.

Turakhia Y., De Maio N., Thornlow B., Gozashti L., Lanfear R., Walker C. R., Hinrichs A. S., Fernandes J. D., Borges R., Slodkiewicz G., Weilguny L., Haussler D., Goldman N., Corbett-Detig R.

[PLOS Genetics 16, e1009175](#) (2020).

A phylodynamic workflow to rapidly gain insights into the dispersal history and dynamics of SARS-CoV-2 lineages.

Dellicour S., Durkin K., Hong S. L., Vanmechelen B., Martí-Carreras J., Gill M. S., Meex C., Bontems S., André E., Gilbert M., Walker C. R., De Maio N., Faria N. R., Hadfield J., Hayette M., Bours V., Wawina-Bokalanga T., Artesi M., Baele G., Maes P.

[Molecular Biology and Evolution 38, 1608–1613](#) (2020).

Preprint/equivalent

phastSim: efficient simulation of sequence evolution for pandemic-scale datasets.

De Maio N., Boulton W., Weilguny L., Walker C. R., Turakhia Y., Corbett-Detig R., Goldman N.

[bioRxiv, doi.org/10.1101/2021.03.15.435416](#) (2021).

Masking strategies for SARS-CoV-2 alignments.

De Maio N., Walker C. R., Borges R., Weilguny L., Slodkiewicz G., Goldman N.

[virological.org/t/masking-strategies-for-sars-cov-2-alignments/480](#) (2020).

Issues with SARS-CoV-2 sequencing data.

De Maio N., Walker C. R., Borges R., Weilguny L., Slodkiewicz G., Goldman N.

[virological.org/t/issues-with-sars-cov-2-sequencing-data/473](#) (2020).

Selected presentations

ISMB/ECCB 2021

Jul. 2021

Talk: Accurate detection of positive selection using convolutional neural networks

Walker C. R., De Maio N., Goldman N.

SMBE 2021

Jul. 2021

Talk: Accurate detection of positive selection using convolutional neural networks

Walker C. R., De Maio N., Goldman N.

Evolution 2021

Jun. 2021

Talk: Accurate detection of positive selection using convolutional neural networks

Walker C. R., De Maio N., Goldman N.

SMBE 2019

Jul. 2019

Poster: Short template switches explain mutation clusters in the human genome

Walker C. R., De Maio N., Goldman N.

EMBL-EBI PhD Seminar Day

May 2019

Talk: Short-range template switching in the human genome

Walker C. R.

NIHR BRC Annual Research Day

Jul. 2018

Talk: Investigating short template switch mutations in humans and model organisms

Walker C. R.

Phylogroup XI

Mar. 2018

Talk: Short template switch events explain mutation clusters in the human genome

Walker C. R., Löytynoja A., Goldman N.

Teaching

Students supervised

- Fatma Rabia Fidan 2021
- Masters-level project: Identifying *de novo* template switch mutations in trios of human genomes
- Shayesteh Arasti (co-advised with Nicola De Maio) 2021
- Masters-level project: Using convolutional neural networks to detect positive selection
- Viacheslav Vasilev (co-advised with Nicola De Maio) 2020
- Masters-level project: Using convolutional neural networks to detect positive selection
- William Xu (co-advised with Nicola De Maio) 2020
- Masters-level project: Using convolutional neural networks to detect positive selection

Teaching assistant

- Medics to Coders · University of Cambridge, UK 2018
- I helped to deliver practical sessions on programming in Python at the School of Clinical Medicine

Honours and awards

- Best student talk May 2019
- Audience vote at the annual EMBL-EBI PhD Seminar Day
- Outstanding performance by a MSc Bioinformatics programme student Oct. 2017
- Awarded for achieving the highest overall grade on my master's degree programme
- Zoology prize Sep. 2016
- Awarded for achieving the highest overall grade on my bachelor's degree programme

Other scientific activities

Committees

- Student Representative · EMBL-EBI, UK 2018-2020
- Attended meetings with senior management from across all EMBL outstations to discuss issues impacting the graduate community at EMBL
 - Organised a variety of academic and social events within the institution
- Graduate Student and Post-Doc Forum member · University of Cambridge, UK 2018
- I worked as part of a group of students and postdocs to devise strategies for creating a more positive experience for graduate students in the School of Life Sciences

Memberships

International Society for Computational Biology
Society for Molecular Biology and Evolution
Society for the Study of Evolution

Reviewer for

Nature Medicine
Molecular Biology and Evolution
BMC Bioinformatics

Skills

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| Programming | Python, Bash, C++, R, AWK, LaTeX |
| Libraries | Numpy, SciPy, Keras, TensorFlow, PyTorch, scikit-allel, matplotlib, seaborn |
| Coding practices | Git, Snakemake, unit testing, Docker, Singularity, Jupyter, Vim |
| High performance computing | Daily use of both CPU and GPU clusters in a LSF environment |
| Operating systems | Linux, MacOS |